

Ungar

CRF Errors Corrected by the STIC Systems Branch

Serial Number:

08/482,402A

CRF Processing Date: 9/10/2001

Edited by:

Verified by:

(STIC stat

ENTERED

☐

Changed a file from non-ASCII to ASCII

☐

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐

Edited a format error in the Current Application Data section, specifically:

☐

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_

☐

Added the mandatory heading and subheadings for "Current Application Data".

☐

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

☐

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☐

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐

Inserted colons after headings/subheadings. Headings edited included:

☐

Deleted extra, invalid, headings-used by an applicant, specifically:

☐

Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_

☐

Inserted mandatory headings, specifically:

☒

Corrected an obvious error in the response, specifically:

41507 response

☐

Edited identifiers where upper case is used but lower case is required, or vice versa.

☐

Corrected an error in the Number of Sequences field, specifically:

☐

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐

Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected:

☐

Other:

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

## RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/08/482,402A

TIME: 16:06:27

Input Set : A:\Pto.amc

Output Set: N:\CRF3\09102001\H482402A.raw

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3 <110> APPLICANT: Rapoport, Basil
5 <120> TITLE OF INVENTION: DISEASE ASSOCIATED HUMAN AUTOANTIBODIES SPECIFIC FOR HUMAN
THYROID
6     PEROXIDASE
8 <130> FILE REFERENCE: A1697DIV3
10 <140> CURRENT APPLICATION NUMBER: 08/482,402A
11 <141> CURRENT FILING DATE: 1996-06-07
13 <150> PRIOR APPLICATION NUMBER: US 08/196,082
14 <151> PRIOR FILING DATE: 1994-03-03
16 <150> PRIOR APPLICATION NUMBER: US 08/182,117
17 <151> PRIOR FILING DATE: 1994-01-27
19 <150> PRIOR APPLICATION NUMBER: PCT/US92/07381
20 <151> PRIOR FILING DATE: 1992-08-28
22 <150> PRIOR APPLICATION NUMBER: PCT/US92/06283
23 <151> PRIOR FILING DATE: 1992-07-30
25 <150> PRIOR APPLICATION NUMBER: US 07/750,579
26 <151> PRIOR FILING DATE: 1991-08-28
28 <150> PRIOR APPLICATION NUMBER: US 07/738,040
29 <151> PRIOR FILING DATE: 1991-07-30
31 <150> PRIOR APPLICATION NUMBER: US 07/559,955
32 <151> PRIOR FILING DATE: 1990-07-31
34 <150> PRIOR APPLICATION NUMBER: US 07/472,070
35 <151> PRIOR FILING DATE: 1990-01-30
37 <150> PRIOR APPLICATION NUMBER: US 07/388,044
38 <151> PRIOR FILING DATE: 1989-07-31
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63 <223> OTHER INFORMATION:
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69 gttggctgag aagaggaaaa aaga atg aga gcg ctg gct gtg ctg tct gtc          111
70                                     Met Arg Ala Leu Ala Val Leu Ser Val
71                                     1             5
73 acg ctg gtt atg gcc tgc aca gaa gcc ttc ttc ccc ttc atc tcg aga          159

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78 Gly Lys Glu Leu Leu Trp Gly Lys Pro Glu Glu Ser Arg Val Ser Ser
79 30 35 40
81 gtc ttg gag gaa agc aag cgc ctg gtg gac acc gcc atg tac gcc acg 255
82 Val Leu Glu Glu Ser Lys Arg Leu Val Asp Thr Ala Met Tyr Ala Thr
83 45 50 55
85 atg cag aga aac ctc aag aaa aga gga atc ctt tct gga gct cag ctt 303
86 Met Gln Arg Asn Leu Lys Lys Arg Gly Ile Leu Ser Gly Ala Gln Leu
87 60 65 70
89 ctg tct ttt tcc aaa ctt cct gag cca aca agc gga gtg att gcc cga 351
90 Leu Ser Phe Ser Lys Leu Pro Glu Pro Thr Ser Gly Val Ile Ala Arg
91 75 80 85
93 gca gca gag ata atg gaa aca tca ata caa gcg atg aaa aga aaa gtc 399
94 Ala Ala Glu Ile Met Glu Thr Ser Ile Gln Ala Met Lys Arg Lys Val
95 90 95 100 105
97 aac ctg aaa act caa caa tca cag cat cca acg gat gct tta tca gaa 447
98 Asn Leu Lys Thr Gln Gln Ser Gln His Pro Thr Asp Ala Leu Ser Glu
99 110 115 120
101 gat ctg ctg agc atc att gca aac atg tct gga tgt ctc cct tac atg 495
102 Asp Leu Leu Ser Ile Ile Ala Asn Met Ser Gly Cys Leu Pro Tyr Met
103 125 130 135
105 ctg ccc cca aaa tgc cca aac act tgc ctg gcg aac aaa tac agg ccc 543
106 Leu Pro Pro Lys Cys Pro Asn Thr Cys Leu Ala Asn Lys Tyr Arg Pro
107 140 145 150
109 atc aca gga gct tgc aac aac aga gac cac ccc aga tgg ggc gcc tcc 591
110 Ile Thr Gly Ala Cys Asn Asn Arg Asp His Pro Arg Trp Gly Ala Ser
111 155 160 165
113 aac acg gcc ctg gca cga tgg ctc cct cca gtc tat gag gac ggc ttc 639
114 Asn Thr Ala Leu Ala Arg Trp Leu Pro Pro Val Tyr Glu Asp Gly Phe
115 170 175 180 185
117 agt cag ccc cga ggc tgg aac ccc ggc ttc ttg tac aac ggg ttc cca 687
118 Ser Gln Pro Arg Gly Trp Asn Pro Gly Phe Leu Tyr Asn Gly Phe Pro
119 190 195 200
121 ctg ccc ccg gtc cgg gag gtg aca aga cat gtc att caa gtt tca aat 735
122 Leu Pro Pro Val Arg Glu Val Thr Arg His Val Ile Gln Val Ser Asn
123 205 210 215
125 gag gtt gtc aca gat gat gac cgc tat tct gac ctc ctg atg gca tgg 783
126 Glu Val Val Thr Asp Asp Asp Arg Tyr Ser Asp Leu Leu Met Ala Trp
127 220 225 230
129 gga caa tac atc gac cac gac atc gcg ttc aca cca cag agc acc agc 831
130 Gly Gln Tyr Ile Asp His Asp Ile Ala Phe Thr Pro Gln Ser Thr Ser
131 235 240 245
133 aaa gct gcc ttc ggg gga ggg tct gac tgc cag atg act tgt gag aac 879
134 Lys Ala Ala Phe Gly Gly Gly Ser Asp Cys Gln Met Thr Cys Glu Asn
135 250 255 260 265
137 caa aac cca tgt ttt ccc ata caa ctc ccg gag gag gcc cgg ccg gcc 927
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142	Ala Gly Thr Ala	Cys Leu Pro Phe Tyr	Arg Ser Ser Ala	Ala Cys Gly				
143		285		290		295		
145	acc ggg gac caa	ggc gcg ctc ttt	ggg aac ctg tcc	acg gcc aac ccg		1023		
146	Thr Gly Asp Gln	Gly Ala Leu Phe Gly	Asn Leu Ser Thr	Ala Asn Pro				
147		300		305		310		
149	agg cag cag atg	aac ggg ttg acc	tcg ttc ctg gac	gcg tcc acc gtg		1071		
150	Arg Gln Gln Met	Asn Gly Leu Thr	Ser Phe Leu Asp	Ala Ser Thr Val				
151		315		320		325		
153	tat ggc agc tcc	ccg gcc cta gag	agg cag ctg cgg	aac tgg acc agt		1119		
154	Tyr Gly Ser Ser	Pro Ala Leu Glu	Arg Gln Leu Arg	Asn Trp Thr Ser				
155	330		335		340		345	
157	gcc gaa ggg ctg	ctc cgc gtc cac	ggc cgc ctc cgg	gac tcc ggc cgc		1167		
158	Ala Glu Gly Leu	Leu Arg Val His	Gly Arg Leu Arg	Asp Ser Gly Arg				
159		350		355		360		
161	gcc tac ctg ccc	ttc gtg ccg cca	cgc gcg cct gcg	gcc tgt gcg ccc		1215		
162	Ala Tyr Leu Pro	Phe Val Pro Pro	Arg Ala Pro Ala	Ala Cys Ala Pro				
163		365		370		375		
165	gag ccc ggc aac	ccc gga gag acc	cgc ggg ccc tgc	ttc ctg gcc gga		1263		
166	Glu Pro Gly Asn	Pro Gly Glu Thr	Arg Gly Pro Cys	Phe Leu Ala Gly				
167		380		385		390		
169	gac ggc cgc gcc	agc gag gtc ccc	tcc ctg acg gca	ctg cac acg ctg		1311		
170	Asp Gly Arg Ala	Ser Glu Val Pro	Ser Leu Thr Ala	Leu His Thr Leu				
171		395		400		405		
173	tgg ctg cgc gag	cac aac cgc ctg	gcc gcg gcg ctc	aag gcc ctc aat		1359		
174	Trp Leu Arg Glu	His Asn Arg Leu	Ala Ala Leu Lys	Ala Leu Asn				
175	410		415		420		425	
177	gcg cac tgg agc	gcg gac gcc gtg	tac cag gag gcg	cgc aag gtc gtg		1407		
178	Ala His Trp Ser	Ala Asp Ala Val	Tyr Gln Glu Ala	Arg Lys Val Val				
179		430		435		440		
181	ggc gct ctg cac	cag atc atc acc	ctg agg gat tac	atc ccc agg atc		1455		
182	Gly Ala Leu His	Gln Ile Ile Thr	Leu Arg Asp Tyr	Ile Pro Arg Ile				
183		445		450		455		
185	ctg gga ccc gag	gcc ttc cag cag	tac gtg ggt ccc	tat gaa ggc tat		1503		
186	Leu Gly Pro Glu	Ala Phe Gln Gln	Tyr Val Gly Pro	Tyr Glu Gly Tyr				
187		460		465		470		
189	gac tcc acc gcc	aac ccc act gtg	tcc aac gtg ttc	tcc aca gcc gcc		1551		
190	Asp Ser Thr Ala	Asn Pro Thr Val	Ser Asn Val Phe	Ser Thr Ala Ala				
191		475		480		485		
193	ttc cgc ttc ggc	cat gcc acg atc	cac ccg ctg gtg	agg agg ctg gac		1599		
194	Phe Arg Phe Gly	His Ala Thr Ile	His Pro Leu Val	Arg Arg Leu Asp				
195	490		495		500		505	
197	gcc agc ttc cag	gag cac ccc gac	ctg ccc ggg ctg	tgg ctg cac cag		1647		
198	Ala Ser Phe Gln	Glu His Pro Asp	Leu Pro Gly Leu	Trp Leu His Gln				
199		510		515		520		
201	gct ttc ttc agc	cca tgg aca tta	ctc cgt gga ggt	ggt ttg gac cca		1695		
202	Ala Phe Phe Ser	Pro Trp Thr Leu	Leu Arg Gly Gly	Gly Leu Asp Pro				
203		525		530		535		

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205	cta	ata	cga	ggc	ctt	ctt	gca	aga	cca	gcc	aaa	ctg	cag	gtg	cag	gat	1743
206	Leu	Ile	Arg	Gly	Leu	Leu	Ala	Arg	Pro	Ala	Lys	Leu	Gln	Val	Gln	Asp	
207			540					545					550				
209	cag	ctg	atg	aac	gag	gag	ctg	acg	gaa	agg	ctc	ttt	gtg	ctg	tcc	aat	1791
210	Gln	Leu	Met	Asn	Glu	Glu	Leu	Thr	Glu	Arg	Leu	Phe	Val	Leu	Ser	Asn	
211			555				560					565					
213	tcc	agc	acc	ttg	gat	ctg	gcg	tcc	atc	aac	ctg	cag	agg	ggc	cgg	gac	1839
214	Ser	Ser	Thr	Leu	Asp	Leu	Ala	Ser	Ile	Asn	Leu	Gln	Arg	Gly	Arg	Asp	
215	570					575					580				585		
217	cac	ggg	ctg	cca	ggt	tac	aat	gag	tgg	agg	gag	ttc	tgc	ggc	ctg	cct	1887
218	His	Gly	Leu	Pro	Gly	Tyr	Asn	Glu	Trp	Arg	Glu	Phe	Cys	Gly	Leu	Pro	
219				590					595					600			
221	cgc	ctg	gag	acc	ccc	gct	gac	ctg	agc	aca	gcc	atc	gcc	agc	agg	agc	1935
222	Arg	Leu	Glu	Thr	Pro	Ala	Asp	Leu	Ser	Thr	Ala	Ile	Ala	Ser	Arg	Ser	
223				605				610					615				
225	gtg	gcc	gac	aag	atc	ctg	gac	ttg	tac	aag	cat	cct	gac	aac	atc	gat	1983
226	Val	Ala	Asp	Lys	Ile	Leu	Asp	Leu	Tyr	Lys	His	Pro	Asp	Asn	Ile	Asp	
227			620				625					630					
229	gtc	tgg	ctg	gga	ggc	tta	gct	gaa	aac	ttc	ctc	ccc	agg	gct	cgg	aca	2031
230	Val	Trp	Leu	Gly	Gly	Leu	Ala	Glu	Asn	Phe	Leu	Pro	Arg	Ala	Arg	Thr	
231			635				640					645					
233	ggg	ccc	ctg	ttt	gcc	tgt	ctc	att	ggg	aag	cag	atg	aag	gct	ctg	cgg	2079
234	Gly	Pro	Leu	Phe	Ala	Cys	Leu	Ile	Gly	Lys	Gln	Met	Lys	Ala	Leu	Arg	
235	650				655				660				665				
237	gac	ggt	gac	tgg	ttt	tgg	tgg	gag	aac	agc	cac	gtc	ttc	acg	gat	gca	2127
238	Asp	Gly	Asp	Trp	Phe	Trp	Trp	Glu	Asn	Ser	His	Val	Phe	Thr	Asp	Ala	
239				670					675				680				
241	cag	agg	cgt	gag	ctg	gag	aag	cac	tcc	ctg	tct	cgg	gtc	atc	tgt	gac	2175
242	Gln	Arg	Arg	Glu	Leu	Glu	Lys	His	Ser	Leu	Ser	Arg	Val	Ile	Cys	Asp	
243			685					690					695				
245	aac	act	ggc	ctc	acc	agg	gtg	ccc	atg	gat	gcc	ttc	caa	gtc	ggc	aaa	2223
246	Asn	Thr	Gly	Leu	Thr	Arg	Val	Pro	Met	Asp	Ala	Phe	Gln	Val	Gly	Lys	
247			700				705					710					
249	ttc	ccc	gaa	gac	ttt	gag	tct	tgt	gac	agc	atc	act	ggc	atg	aac	ctg	2271
250	Phe	Pro	Glu	Asp	Phe	Glu	Ser	Cys	Asp	Ser	Ile	Thr	Gly	Met	Asn	Leu	
251			715				720					725					
253	gag	gcc	tgg	agg	gaa	acc	ttt	cct	caa	gac	gac	aag	tgt	ggc	ttc	cca	2319
254	Glu	Ala	Trp	Arg	Glu	Thr	Phe	Pro	Gln	Asp	Asp	Lys	Cys	Gly	Phe	Pro	
255	730				735				740				745				
257	gag	agc	gtg	gag	aat	ggg	gac	ttt	gtg	cac	tgt	gag	gag	tct	ggg	agg	2367
258	Glu	Ser	Val	Glu	Asn	Gly	Asp	Phe	Val	His	Cys	Glu	Glu	Ser	Gly	Arg	
259				750				755					760				
261	cgc	gtg	ctg	gtg	tat	tcc	tgc	cgg	cac	ggg	tat	gag	ctc	caa	ggc	cgg	2415
262	Arg	Val	Leu	Val	Tyr	Ser	Cys	Arg	His	Gly	Tyr	Glu	Leu	Gln	Gly	Arg	
263			765				770					775					
265	gag	cag	ctc	act	tgc	acc	cag	gaa	gga	tgg	gat	ttc	cag	cct	ccc	ctc	2463
266	Glu	Gln	Leu	Thr	Cys	Thr	Gln	Glu	Gly	Trp	Asp	Phe	Gln	Pro	Pro	Leu	
267			780				785					790					
269	tgc	aaa	gat	gtg	aac	gag	tgt	gca	gac	ggt	gcc	cac	ccc	ccc	tgc	cac	2511

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Output Set: N:\CRF3\09102001\H482402A.raw

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273 gcc tct gcg agg tgc aga aac acc aaa ggc ggc ttc cag tgt ctc tgc      2559
274 Ala Ser Ala Arg Cys Arg Asn Thr Lys Gly Gly Phe Gln Cys Leu Cys
275 810      815      820      825
277 gcg gac ccc tac gag tta gga gac gat ggg aga acc tgc gta gac tcc      2607
278 Ala Asp Pro Tyr Glu Leu Gly Asp Asp Gly Arg Thr Cys Val Asp Ser
279      830      835      840
281 ggg agg ctc cct cgg gtg act tgg atc tcc atg tcg ctg gct gct ctg      2655
282 Gly Arg Leu Pro Arg Val Thr Trp Ile Ser Met Ser Leu Ala Leu
283      845      850      855
285 ctg atc gga ggc ttc gca ggt ctc acc tcg acg gtg att tgc agg tgg      2703
286 Leu Ile Gly Gly Phe Ala Gly Leu Thr Ser Thr Val Ile Cys Arg Trp
287      860      865      870
289 aca cgc act ggc act aaa tcc aca ctg ccc atc tcg gag aca ggc gga      2751
290 Thr Arg Thr Gly Thr Lys Ser Thr Leu Pro Ile Ser Glu Thr Gly Gly
291      875      880      885
293 gga act ccc gag ctg aga tgc gga aag cac cag gcc gta ggg acc tca      2799
294 Gly Thr Pro Glu Leu Arg Cys Gly Lys His Gln Ala Val Gly Thr Ser
295 890      895      900      905
297 ccg cag cgg gcc gca gct cag gac tcg gag cag gag agt gct ggg atg      2847
298 Pro Gln Arg Ala Ala Ala Gln Asp Ser Glu Gln Glu Ser Ala Gly Met
299      910      915      920
301 gaa ggc cgg gat act cac agg ctg ccg aga gcc ctc tgagggcaaa      2893
302 Glu Gly Arg Asp Thr His Arg Leu Pro Arg Ala Leu
303      925      930
305 gtggcaggac actgcagaac agcttcatgt tcccaaaatc accgtacgac tcttttccaa      2953
307 acacaggcaa atcggaaatc agcaggacga ctgttttccc aacacgggta aatctagtac      3013
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324      20      25      30
327 Lys Pro Glu Glu Ser Arg Val Ser Ser Val Leu Glu Glu Ser Lys Arg
328      35      40      45
331 Leu Val Asp Thr Ala Met Tyr Ala Thr Met Gln Arg Asn Leu Lys Lys
332      50      55      60
335 Arg Gly Ile Leu Ser Gly Ala Gln Leu Leu Ser Phe Ser Lys Leu Pro
336 65      70      75      80
339 Glu Pro Thr Ser Gly Val Ile Ala Arg Ala Ala Glu Ile Met Glu Thr
340      85      90      95
343 Ser Ile Gln Ala Met Lys Arg Lys Val Asn Leu Lys Thr Gln Gln Ser
344      100      105      110
347 Gln His Pro Thr Asp Ala Leu Ser Glu Asp Leu Leu Ser Ile Ile Ala

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VERIFICATION SUMMARY

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OIPE

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DATE: 08/29/2001

PATENT APPLICATION: US/08/482,402A

TIME: 14:17:39

Input Set : A:\ES.txt

Output Set: N:\CRF3\08292001\H482402A.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Rapoport, Basil  
 5 <120> TITLE OF INVENTION: DISEASE ASSOCIATED HUMAN AUTOANTIBODIES SPECIFIC FOR HUMAN  
 THYROID  
 6 PEROXIDASE  
 8 <130> FILE REFERENCE: A1697DIV3  
 10 <140> CURRENT APPLICATION NUMBER: 08/482,402A  
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 38 <151> PRIOR FILING DATE: 1989-07-31  
 40 <160> NUMBER OF SEQ ID NOS: 12  
 42 <170> SOFTWARE: PatentIn version 3.1  
 44 <210> SEQ ID NO: 1  
 45 <211> LENGTH: 104  
 46 <212> TYPE: DNA  
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 70 Met Arg Ala Leu Ala Val Leu Ser Val  
 71 1 5  
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Input Set : A:\ES.txt

Output Set: N:\CRF3\08292001\H482402A.raw

74	Thr	Leu	Val	Met	Ala	Cys	Thr	Glu	Ala	Phe	Phe	Pro	Phe	Ile	Ser	Arg	
75	10					15					20					25	
77	ggg	aaa	gaa	ctc	ctt	tgg	gga	aag	cct	gag	gag	tct	cgt	gtc	tct	agc	207
78	Gly	Lys	Glu	Leu	Leu	Trp	Gly	Lys	Pro	Glu	Glu	Ser	Arg	Val	Ser	Ser	
79					30					35				40			
81	gtc	ttg	gag	gaa	agc	aag	cgc	ctg	gtg	gac	acc	gcc	atg	tac	gcc	acg	255
82	Val	Leu	Glu	Glu	Ser	Lys	Arg	Leu	Val	Asp	Thr	Ala	Met	Tyr	Ala	Thr	
83				45				50					55				
85	atg	cag	aga	aac	ctc	aag	aaa	aga	gga	atc	ctt	tct	gga	gct	cag	ctt	303
86	Met	Gln	Arg	Asn	Leu	Lys	Lys	Arg	Gly	Ile	Leu	Ser	Gly	Ala	Gln	Leu	
87		60						65				70					
89	ctg	tct	ttt	tcc	aaa	ctt	cct	gag	cca	aca	agc	gga	gtg	att	gcc	cga	351
90	Leu	Ser	Phe	Ser	Lys	Leu	Pro	Glu	Pro	Thr	Ser	Gly	Val	Ile	Ala	Arg	
91		75					80					85					
93	gca	gca	gag	ata	atg	gaa	aca	tca	ata	caa	gcg	atg	aaa	aga	aaa	gtc	399
94	Ala	Ala	Glu	Ile	Met	Glu	Thr	Ser	Ile	Gln	Ala	Met	Lys	Arg	Lys	Val	
95	90				95					100					105		
97	aac	ctg	aaa	act	caa	caa	tca	cag	cat	cca	acg	gat	gct	tta	tca	gaa	447
98	Asn	Leu	Lys	Thr	Gln	Gln	Ser	Gln	His	Pro	Thr	Asp	Ala	Leu	Ser	Glu	
99				110				115					120				
101	gat	ctg	ctg	agc	atc	att	gca	aac	atg	tct	gga	tgt	ctc	cct	tac	atg	495
102	Asp	Leu	Leu	Ser	Ile	Ile	Ala	Asn	Met	Ser	Gly	Cys	Leu	Pro	Tyr	Met	
103				125				130					135				
105	ctg	ccc	cca	aaa	tgc	cca	aac	act	tgc	ctg	gcg	aac	aaa	tac	agg	ccc	543
106	Leu	Pro	Pro	Lys	Cys	Pro	Asn	Thr	Cys	Leu	Ala	Asn	Lys	Tyr	Arg	Pro	
107				140				145					150				
109	atc	aca	gga	gct	tgc	aac	aac	aga	gac	cac	ccc	aga	tgg	ggc	gcc	tcc	591
110	Ile	Thr	Gly	Ala	Cys	Asn	Asn	Arg	Asp	His	Pro	Arg	Trp	Gly	Ala	Ser	
111		155					160					165					
113	aac	acg	gcc	ctg	gca	cga	tgg	ctc	cct	cca	gtc	tat	gag	gac	ggc	ttc	639
114	Asn	Thr	Ala	Leu	Ala	Arg	Trp	Leu	Pro	Pro	Val	Tyr	Glu	Asp	Gly	Phe	
115	170				175					180					185		
117	agt	cag	ccc	cga	ggc	tgg	aac	ccc	ggc	ttc	ttg	tac	aac	ggg	ttc	cca	687
118	Ser	Gln	Pro	Arg	Gly	Trp	Asn	Pro	Gly	Phe	Leu	Tyr	Asn	Gly	Phe	Pro	
119				190				195					200				
121	ctg	ccc	ccg	gtc	cgg	gag	gtg	aca	aga	cat	gtc	att	caa	gtt	tca	aat	735
122	Leu	Pro	Pro	Val	Arg	Glu	Val	Thr	Arg	His	Val	Ile	Gln	Val	Ser	Asn	
123				205				210					215				
125	gag	gtt	gtc	aca	gat	gat	gac	cgc	tat	tct	gac	ctc	ctg	atg	gca	tgg	783
126	Glu	Val	Val	Thr	Asp	Asp	Asp	Arg	Tyr	Ser	Asp	Leu	Leu	Met	Ala	Trp	
127				220				225					230				
129	gga	caa	tac	atc	gac	cac	gac	atc	gcg	ttc	aca	cca	cag	agc	acc	agc	831
130	Gly	Gln	Tyr	Ile	Asp	His	Asp	Ile	Ala	Phe	Thr	Pro	Gln	Ser	Thr	Ser	
131		235				240						245					
133	aaa	gct	gcc	ttc	ggg	gga	ggg	tct	gac	tgc	cag	atg	act	tgt	gag	aac	879
134	Lys	Ala	Ala	Phe	Gly	Gly	Gly	Ser	Asp	Cys	Gln	Met	Thr	Cys	Glu	Asn	
135	250				255					260					265		
137	caa	aac	cca	tgt	ttt	ccc	ata	caa	ctc	ccg	gag	gag	gcc	cgg	ccg	gcc	927
138	Gln	Asn	Pro	Cys	Phe	Pro	Ile	Gln	Leu	Pro	Glu	Glu	Ala	Arg	Pro	Ala	

## RAW SEQUENCE LISTING

DATE: 08/29/2001

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Input Set : A:\ES.txt

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139		270		275		280	
141	gcg ggc acc gcc tgt ctg ccc ttc tac cgc tct tcg gcc gcc tgc ggc						975
142	Ala Gly Thr Ala Cys Leu Pro Phe Tyr Arg Ser Ser Ala Ala Cys Gly						
143		285		290		295	
145	acc ggg gac caa ggc gcg ctc ttt ggg aac ctg tcc acg gcc aac ccg						1023
146	Thr Gly Asp Gln Gly Ala Leu Phe Gly Asn Leu Ser Thr Ala Asn Pro						
147		300		305		310	
149	agg cag cag atg aac ggg ttg acc tcg ttc ctg gac gcg tcc acc gtg						1071
150	Arg Gln Gln Met Asn Gly Leu Thr Ser Phe Leu Asp Ala Ser Thr Val						
151		315		320		325	
153	tat ggc agc tcc ccg gcc cta gag agg cag ctg cgg aac tgg acc agt						1119
154	Tyr Gly Ser Ser Pro Ala Leu Glu Arg Gln Leu Arg Asn Trp Thr Ser						
155	330		335		340		345
157	gcc gaa ggg ctg ctc cgc gtc cac ggc cgc ctc cgg gac tcc ggc cgc						1167
158	Ala Glu Gly Leu Leu Arg Val His Gly Arg Leu Arg Asp Ser Gly Arg						
159		350		355		360	
161	gcc tac ctg ccc ttc gtg ccg cca cgc gcg cct gcg gcc tgt gcg ccc						1215
162	Ala Tyr Leu Pro Phe Val Pro Pro Arg Ala Pro Ala Ala Cys Ala Pro						
163		365		370		375	
165	gag ccc ggc aac ccc gga gag acc cgc ggg ccc tgc ttc ctg gcc gga						1263
166	Glu Pro Gly Asn Pro Gly Glu Thr Arg Gly Pro Cys Phe Leu Ala Gly						
167		380		385		390	
169	gac ggc cgc gcc agc gag gtc ccc tcc ctg acg gca ctg cac acg ctg						1311
170	Asp Gly Arg Ala Ser Glu Val Pro Ser Leu Thr Ala Leu His Thr Leu						
171		395		400		405	
173	tgg ctg cgc gag cac aac cgc ctg gcc gcg gcg ctc aag gcc ctc aat						1359
174	Trp Leu Arg Glu His Asn Arg Leu Ala Ala Ala Leu Lys Ala Leu Asn						
175	410		415		420		425
177	gcg cac tgg agc gcg gac gcc gtg tac cag gag gcg cgc aag gtc gtg						1407
178	Ala His Trp Ser Ala Asp Ala Val Tyr Gln Glu Ala Arg Lys Val Val						
179		430		435		440	
181	ggc gct ctg cac cag atc atc acc ctg agg gat tac atc ccc agg atc						1455
182	Gly Ala Leu His Gln Ile Ile Thr Leu Arg Asp Tyr Ile Pro Arg Ile						
183		445		450		455	
185	ctg gga ccc gag gcc ttc cag cag tac gtg ggt ccc tat gaa ggc tat						1503
186	Leu Gly Pro Glu Ala Phe Gln Gln Tyr Val Gly Pro Tyr Glu Gly Tyr						
187		460		465		470	
189	gac tcc acc gcc aac ccc act gtg tcc aac gtg ttc tcc aca gcc gcc						1551
190	Asp Ser Thr Ala Asn Pro Thr Val Ser Asn Val Phe Ser Thr Ala Ala						
191		475		480		485	
193	ttc cgc ttc ggc cat gcc acg atc cac ccg ctg gtg agg agg ctg gac						1599
194	Phe Arg Phe Gly His Ala Thr Ile His Pro Leu Val Arg Arg Leu Asp						
195	490		495		500		505
197	gcc agc ttc cag gag cac ccc gac ctg ccc ggg ctg tgg ctg cac cag						1647
198	Ala Ser Phe Gln Glu His Pro Asp Leu Pro Gly Leu Trp Leu His Gln						
199		510		515		520	
201	gct ttc ttc agc cca tgg aca tta ctc cgt gga ggt ggt ttg gac cca						1695
202	Ala Phe Phe Ser Pro Trp Thr Leu Leu Arg Gly Gly Gly Leu Asp Pro						
203		525		530		535	

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205	cta	ata	cga	ggc	ctt	ctt	gca	aga	cca	gcc	aaa	ctg	cag	gtg	cag	gat	1743
206	Leu	Ile	Arg	Gly	Leu	Leu	Ala	Arg	Pro	Ala	Lys	Leu	Gln	Val	Gln	Asp	
207			540					545					550				
209	cag	ctg	atg	aac	gag	gag	ctg	acg	gaa	agg	ctc	ttt	gtg	ctg	tcc	aat	1791
210	Gln	Leu	Met	Asn	Glu	Glu	Leu	Thr	Glu	Arg	Leu	Phe	Val	Leu	Ser	Asn	
211			555				560					565					
213	tcc	agc	acc	ttg	gat	ctg	gcg	tcc	atc	aac	ctg	cag	agg	ggc	cgg	gac	1839
214	Ser	Ser	Thr	Leu	Asp	Leu	Ala	Ser	Ile	Asn	Leu	Gln	Arg	Gly	Arg	Asp	
215	570					575				580					585		
217	cac	ggg	ctg	cca	ggt	tac	aat	gag	tgg	agg	gag	ttc	tgc	ggc	ctg	cct	1887
218	His	Gly	Leu	Pro	Gly	Tyr	Asn	Glu	Trp	Arg	Glu	Phe	Cys	Gly	Leu	Pro	
219					590					595					600		
221	cgc	ctg	gag	acc	ccc	gct	gac	ctg	agc	aca	gcc	atc	gcc	agc	agg	agc	1935
222	Arg	Leu	Glu	Thr	Pro	Ala	Asp	Leu	Ser	Thr	Ala	Ile	Ala	Ser	Arg	Ser	
223				605						610					615		
225	gtg	gcc	gac	aag	atc	ctg	gac	ttg	tac	aag	cat	cct	gac	aac	atc	gat	1983
226	Val	Ala	Asp	Lys	Ile	Leu	Asp	Leu	Tyr	Lys	His	Pro	Asp	Asn	Ile	Asp	
227			620				625						630				
229	gtc	tgg	ctg	gga	ggc	tta	gct	gaa	aac	ttc	ctc	ccc	agg	gct	cgg	aca	2031
230	Val	Trp	Leu	Gly	Gly	Leu	Ala	Glu	Asn	Phe	Leu	Pro	Arg	Ala	Arg	Thr	
231			635				640						645				
233	ggg	ccc	ctg	ttt	gcc	tgt	ctc	att	ggg	aag	cag	atg	aag	gct	ctg	cgg	2079
234	Gly	Pro	Leu	Phe	Ala	Cys	Leu	Ile	Gly	Lys	Gln	Met	Lys	Ala	Leu	Arg	
235	650				655					660					665		
237	gac	ggt	gac	tgg	ttt	tgg	tgg	gag	aac	agc	cac	gtc	ttc	acg	gat	gca	2127
238	Asp	Gly	Asp	Trp	Phe	Trp	Trp	Glu	Asn	Ser	His	Val	Phe	Thr	Asp	Ala	
239					670					675					680		
241	cag	agg	cgt	gag	ctg	gag	aag	cac	tcc	ctg	tct	cgg	gtc	atc	tgt	gac	2175
242	Gln	Arg	Arg	Glu	Leu	Glu	Lys	His	Ser	Leu	Ser	Arg	Val	Ile	Cys	Asp	
243				685					690						695		
245	aac	act	ggc	ctc	acc	agg	gtg	ccc	atg	gat	gcc	ttc	caa	gtc	ggc	aaa	2223
246	Asn	Thr	Gly	Leu	Thr	Arg	Val	Pro	Met	Asp	Ala	Phe	Gln	Val	Gly	Lys	
247			700						705						710		
249	ttc	ccc	gaa	gac	ttt	gag	tct	tgt	gac	agc	atc	act	ggc	atg	aac	ctg	2271
250	Phe	Pro	Glu	Asp	Phe	Glu	Ser	Cys	Asp	Ser	Ile	Thr	Gly	Met	Asn	Leu	
251			715				720						725				
253	gag	gcc	tgg	agg	gaa	acc	ttt	cct	caa	gac	gac	aag	tgt	ggc	ttc	cca	2319
254	Glu	Ala	Trp	Arg	Glu	Thr	Phe	Pro	Gln	Asp	Asp	Lys	Cys	Gly	Phe	Pro	
255	730					735						740				745	
257	gag	agc	gtg	gag	aat	ggg	gac	ttt	gtg	cac	tgt	gag	gag	tct	ggg	agg	2367
258	Glu	Ser	Val	Glu	Asn	Gly	Asp	Phe	Val	His	Cys	Glu	Glu	Ser	Gly	Arg	
259					750					755					760		
261	cgc	gtg	ctg	gtg	tat	tcc	tgc	cgg	cac	ggg	tat	gag	ctc	caa	ggc	cgg	2415
262	Arg	Val	Leu	Val	Tyr	Ser	Cys	Arg	His	Gly	Tyr	Glu	Leu	Gln	Gly	Arg	
263					765					770					775		
265	gag	cag	ctc	act	tgc	acc	cag	gaa	gga	tgg	gat	ttc	cag	cct	ccc	ctc	2463
266	Glu	Gln	Leu	Thr	Cys	Thr	Gln	Glu	Gly	Trp	Asp	Phe	Gln	Pro	Pro	Leu	
267			780							785					790		
269	tgc	aaa	gat	gtg	aac	gag	tgt	gca	gac	ggt	gcc	cac	ccc	ccc	tgc	cac	2511

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Input Set : A:\ES.txt

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270 Cys Lys Asp Val Asn Glu Cys Ala Asp Gly Ala His Pro Pro Cys His
271      795      800      805
273 gcc tct gcg agg tgc aga aac acc aaa ggc ggc ttc cag tgt ctc tgc      2559
274 Ala Ser Ala Arg Cys Arg Asn Thr Lys Gly Gly Phe Gln Cys Leu Cys
275 810      815      820      825
277 gcg gac ccc tac gag tta gga gac gat ggg aga acc tgc gta gac tcc      2607
278 Ala Asp Pro Tyr Glu Leu Gly Asp Asp Gly Arg Thr Cys Val Asp Ser
279      830      835      840
281 ggg agg ctc cct cgg gtg act tgg atc tcc atg tcg ctg gct gct ctg      2655
282 Gly Arg Leu Pro Arg Val Thr Trp Ile Ser Met Ser Leu Ala Ala Leu
283      845      850      855
285 ctg atc gga ggc ttc gca ggt ctc acc tcg acg gtg att tgc agg tgg      2703
286 Leu Ile Gly Gly Phe Ala Gly Leu Thr Ser Thr Val Ile Cys Arg Trp
287      860      865      870
289 aca cgc act ggc act aaa tcc aca ctg ccc atc tcg gag aca ggc gga      2751
290 Thr Arg Thr Gly Thr Lys Ser Thr Leu Pro Ile Ser Glu Thr Gly Gly
291      875      880      885
293 gga act ccc gag ctg aga tgc gga aag cac cag gcc gta ggg acc tca      2799
294 Gly Thr Pro Glu Leu Arg Cys Gly Lys His Gln Ala Val Gly Thr Ser
295 890      895      900      905
297 ccg cag cgg gcc gca gct cag gac tcg gag cag gag agt gct ggg atg      2847
298 Pro Gln Arg Ala Ala Ala Gln Asp Ser Glu Gln Glu Ser Ala Gly Met
299      910      915      920
301 gaa ggc cgg gat act cac agg ctg ccg aga gcc ctc tgagggc aaa      2893
302 Glu Gly Arg Asp Thr His Arg Leu Pro Arg Ala Leu
303      925      930
305 gtggcaggac actgcagaac agcttcatgt tcccaaaatc accgtacgac tcttttccaa      2953
307 acacaggcaa atcggaatc agcaggacga ctgttttccc aacacgggta aatctagtag      3013
309 catgtcgtag ttactctcag gcatggatga ataaatgtta tagctgcaaa aaaaaaaaaa      3072
312 <210> SEQ ID NO: 3
313 <211> LENGTH: 933
314 <212> TYPE: PRT
315 <213> ORGANISM: Homo sapiens
317 <400> SEQUENCE: 3
319 Met Arg Ala Leu Ala Val Leu Ser Val Thr Leu Val Met Ala Cys Thr
320 1      5      10      15
323 Glu Ala Phe Phe Pro Phe Ile Ser Arg Gly Lys Glu Leu Leu Trp Gly
324      20      25      30
327 Lys Pro Glu Glu Ser Arg Val Ser Ser Val Leu Glu Glu Ser Lys Arg
328      35      40      45
331 Leu Val Asp Thr Ala Met Tyr Ala Thr Met Gln Arg Asn Leu Lys Lys
332      50      55      60
335 Arg Gly Ile Leu Ser Gly Ala Gln Leu Leu Ser Phe Ser Lys Leu Pro
336 65      70      75      80
339 Glu Pro Thr Ser Gly Val Ile Ala Arg Ala Ala Glu Ile Met Glu Thr
340      85      90      95
343 Ser Ile Gln Ala Met Lys Arg Lys Val Asn Leu Lys Thr Gln Gln Ser
344      100      105      110
347 Gln His Pro Thr Asp Ala Leu Ser Glu Asp Leu Leu Ser Ile Ile Ala

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VERIFICATION SUMMARY

DATE: 08/29/2001

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Input Set : A:\ES.txt

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